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Perfect score:
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      871
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1: sp_archea:*
2: sp_bacteria:*
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      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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sp_phage:*
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sp_mhc:*
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Q925U7
Q927736
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P70172 mus musculu
Q925u7 mus musculu
O97736 oryctolagus
O35940 mus musculu
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45	44	43	42	41	40	39	38	37	36	35	34	<u>3</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
121	121.5	124	132	142	150	150	156	170	171	173	211	219.5	222.5	223	228.5	230	238.5	239	240	250	257.5	265.5	266	266.5	266.5	269.5	276	277
6.1	6.1	6.3	6.7	7.2	7.6	7.6	7.9	8.6	8.6	8.7	10.7	11.1	11.2	11.3	11.5	11.6	12.1	12.1	12.1	12.6	13.0	13.4	13.4	13.5	13.5	13.6	13.9	14.0
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074395 schizosacch	Q9x0q5 thermotoga	Q8sev7 leptura arc	Q8tmm4 methanosarc	O86662 streptomyce	Q91sv9 arabidopsis	Q8rxe8 arabidopsis			O49665 arabidopsis	Q8vyy4 arabidopsis	Q91xs4 mus musculu	Q8ylp2 anabaena sp	Q9jx64 neisseria m	Q8u766 agrobacteri	Q8zkl0 salmonella		P73938 synechocyst	o.			Q9i375 pseudomonas	Q9jvb5 neisseria m	Q9vxv4 drosophila.	Q8tpb0 methanosarc		Q9hyx6 pseudomonas	Q8s2v7 arabidopsis	Q9asa9 oryza sativ

ALIGNMENTS

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"Functional annotation of a full-length mouse Nature 409:685-690(2001). EMBL; AK018423; BAB31203.1; MGD; MGI:1923000; 8430417G17Rik.	SUZUKI H., TOYO-OKA K., WANG K.H., WEITZ C., Wynshaw-Boris A., Yoshida K., Hasegawa Y., K. Hayashizaki Y.:	Sasaki H., Sato K., Schoenbach C., Seya T.,		RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		Schriml L.M., Staubli F., Suzuki R., Tomit	Fleischmann W., Gaasterland T., Gissi C., Kuehl P., Lewis S., Matsuo Y., Nikaido I.,	Kadota K., Matsuda H.A., Ashburner M., Bata	Saito T., Okazaki Y., Gojobori T., Bono H.,	Aizawa K., Izawa M., Nishi K., Kiyosawa H., I	Arakawa T., Hara A., Fukunishi Y., Konno H.,		MEDLINE=21085660; PubMed=11217851;		RP SEOUENCE FROM N.A.		Mammalia; Eutheria; Rodentia;			GN 843041/G1/RIK PICCEIII.	01-MAR-2002 (T	01-JUN-2001 (TrEMBLrel. 17, Last	01-JUN-2001 (TrEMBLrel. 17, Created)	Q9CXB2;	ID Q9CXB2 PRELIMINARY; PRT; 373 AA.	RESULT 1 Q9CXB2
cDNA collection.";	, Whittaker C., Wilming L., Kawaji H., Kohtsuki S.,	Shibata Y., Storch KF.,	i J., Mombaerts P.,	M., Gariboldi M., Kamiya M., Lee N.H.,	, de Bonaldo M.F.,	, Wagner L., Washio T.,	<pre>King B., Kochiwa H., Pesole G., Quackenbush J.,</pre>	S., Casavant T.,	ito	amanaka	achi J., Fukuda	, Itoh M., Ishii Y.,					•••	rata; Euteleostomi;			date)	te)	•			

448 321 305 318 323 338

Q8wuz2 homo sapien Q96ep9 homo sapien Q8v183 mus musculu Q8qzr2 mus musculu Q9qz12 mesocricetu Q9bs12 homo sapien O34524 bacillus su Q99rv2 staphylococ Q8yiu6 brucella me Q9kej4 bacillus ha O81017 arabidopsis

462 125 473 187

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RESULT
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         Query Match
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Matches 167
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Best Local S
Matches 265
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P70172;
O1-FEB-1997 (TrEMBLrel. 02,
O1-JAN-1998 (TrEMBLrel. 05,
O1-JUN-2002 (TrEMBLrel. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002657;
Pfam; PF01758; SBF; 1
SEQUENCE 373 AA; 4
                                           MGD; MGI:1201406; Slc10a2.
InterPro; IPR004710; Bass.
InterPro; IPR002657; BileAc/Na_smprtr.
Pfam; PF01758; SBF; 1.
TIGRFAMS; TIGR00841; bass; 1.
SEQUENCE 348 AA; 38134 MW; D00B5E4
                                                                                                                                                                Saeki T.,
Submitted
                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                      P70172
                                                                                                 EMBL; AB002693; BAA19606.1; -.
                                                                                                                                       STRAIN=ICR;
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                    Submitted (AUG-1996) to the
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           167;
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                   Similarity
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(APR-1997)
                                                                                                                                               9-332 FROM N.A.
           Conservative
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                      Chordata;
Rodentia;
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70.3%;
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05, Last sequence update)
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e acid transporter (ISBT).
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                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                 EMBL/GenBank/DDBJ
          Score 871; DB 1
Pred. No. 1e-63;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1415;
Pred. No. 2
                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                      PRT;
                                              D00B5E43431875D7
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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167; Conserv
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NYRWPKQSKIILKIGAVVGGVLLLVVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVTGF
                          RRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAIAVLIMGCCPGGTISNIFTFWVDGD
                                                                                                   NSSVCPPNATVCEGDSCVVPESNFNAVLNTVMSSVLTTLLAMVMFSMGCNVEVHKFLGHI
                                                                KRPWGIFVGFLCQFGIMPLTGFILSVASGILPVQAVVVLIMGCCPGGTGSNILAYWIDGD
                                                                                                                     SSSACPANSS--EEELPYGLEVHGN--LELYFTVVSTVMGLLMFSLGCSVEIRKLWSHI
                                                                                                                                        Conservative
                                                                                                                                              43.8%;
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RRPWGIAVGLLCQFGLMPFTAYLLAISFSLKPVQAIAVLIMGCCPGGTISNIFTFWVDGD
VILGIYVTYRK----CYGKNDAEFLE--KTDNEMDSRPSFDETNKGFQPDEK
                                                              FLARLAGQPWYRCRTVALETGMQNTQLCSTIVQLSFSPEDLNLVFTFPLIYTVFQLVFAA
                                                                                    LLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAEHLVQMLSFPLAYGLFQLIDGF
                                                                                                                                NHKWPQKAKIILKIGSITGVILIVLIAVIGGILYQSAWIIEPKLWIIGTIFPIAGYSLGF
                                                                                                                                                 NYRWPKOSKIILKIGAVVGGVLLLUVVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVTGF
                                                                                                                                                                                                                                                                 KRPWGIFVGFLCQFGIMPLTGFILSVASGILPVQAVVVLIMGCCPGGTGSNILAYWIDGD
                             LIVAAYOTYKRRLKNKHGKKNSGCTEVCHTRKSTSSR----ETNAFLEVNEE
 348
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EMBL; AF271073; AAK55514.1; JOINED.
EMBL; AF266724; AAK55514.1; JOINED.
EMBL; AF266725; AAK55514.1; JOINED.
EMBL; AF266725; AAK55514.1; JOINED.
EMBL; AF266726; AAK55514.1; JOINED.
EMBL; AF266727; AAK55514.1; JOINED.
EMBL; AF266728; AAK55514.1; JOINED.
InterPro; IFR004710; Bass.
InterPro; IFR004710; Bass.
InterPro; IFR004671; Bass.
TIGRFAMS; TIGR00841; bass; 1.
SEQUENCE: 348 AA; 38094 MW; AD33A1BC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q925U7
Q925U7;
Q925U7;
Q925U7;
Q1-DEC-2001 (TrEMBLrel. 19, COI-DEC-2001 (TrEMBLrel. 19, LOI-JUN-2002 (TrEMBLrel. 21, LOI-JUN-2002 (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dawson P.A., Craddock A.L., Tietjen M.E., Hayw
"Disruption of the Ileal Bile Acid Transporter
"Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last
Last
acid
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Score 866;
Pred. No. 2.
                                                                                                                                                                                            AD33A1BC76A44482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update) annotation update)
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                                                            DB 11;
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mice.";
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Pred. No. 2.6e 3; Mismatches

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98;

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14;

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182 182 122 122 62 62

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097736
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Matches
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                                                                                                                                                                                       035940;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hepatic sodium-dependent bile acid transporter.
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1998) to the EMBL/GenBank/DDBJ EMBL; AJ131361; CAA10360.1; -.
InterPro; IPR004710; Bass.
InterPro; IPR002657; BlleAc/Na_smprtr.
PF01758; SBF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stengelin S., Becker W
"Rabbit cDNA encoding
transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                      SLC10A1 OR NTCP
                                                                                        Na/taurocholate cotransporting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     NIOMCITMLOLSFTABHLVOMLSFPLAYGLFQLIDGFLIVAAYQTYKR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIYEGDLKDK--VPYGGIMISLVMILIPCTIGIILKSKRPQYVPYVIKVGIIITFSISIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVFTVVSTVMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLLAISF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIVAAYQTYKRRLKNKHGKKNSGCTEVCHTRKSTSSR----ETNAFLEVNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLARLAGQPWYRCRTVALETGMQNTQLCSTIVQLSFSPEDLNLVFTFPLIYTVFQLVFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAEHLVQMLSFPLAYGLFQLIDGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLKPVQAIAVLIMGCCPGGTISNIFTFWVDGDMDLSISMTTCSTVAALGMMPLCIYLYT- 149
                                                                                                                                                                                                                                                                                                                                NVQLCSTILNVTFAPEVIGPLFFFPLLYMIFQLAEGLLIIAVFRCYEK 309
                                                                                                                                                                                                                                                                                                                                                                                                                             VAVLSAINVGNSIMYVMTPYFLTISALMPFIGFLLGFILSALFRLSARCSRTISMETGFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAVAGVVLAKGSWNSDIT---LITISFIFPLIGHVTGFLLALFTHQSWQRCRTISLETGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --WSWSLQQNLTIPYQNIGITLYCLTIPVAFGVYVNYRWPKQSKIILKIGAVVGGVLLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt RMNNIEALAILVCGCSPGGNMSNLFSLAVKGDMNLSIVMTTCSTFLALGMMPLLLYIYSR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLALSVILVIMLLTIMLSLGCTMEFSKIKAHFLKPKGLAIALVAQYGIMPLTAFVLGKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR00841; bass; 1. 348 AA; 37932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                PRELIMINARY;
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  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.9%;
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                                                                                                                   21, 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maier M., Noll R., Kramer W.; patic sodium-dependent bile ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                        Last sequence update)
Last annotation update)
ing polypeptide 2.
                                                                                                                                                                    Created)
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Pred. No. 8.5e-39;
9; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     992A08F4AAA4489B CRC64;
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    BuM
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Best Local S
Matches 118
                                            Matches
                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8WUZ2
Q8WUZ2;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U95132; AAB81024.1; -.
                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019066; AAH19066.1; -
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical 46.5 kDa protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata,
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01758; SBF; 1.
TIGRFAMS; TIGR00841; b
SEQUENCE 317 AA; 34
                                                                                                                                           Hypothetical protein. SEQUENCE 437 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002
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                                                                                                                                                                                       InterPro; IPR002657; BileAc/Na_smprtr
Pfam; PF01758; SBF; 1.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97379; Slc10a1.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR004710; Bass.
nterPro; IPR002657; BileAc/Na_smprtr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE
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                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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118; Conser
    27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIIFRCY-LKIKPQKGK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALFRINDSCRRTISMETGFQNVQLCGTILNVTFPDEVIGPLFFFPLLYMIFQLAEGLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCSTVAALGMMPLCIYLYT---WSWSLQQNLTIPYQNIGITLVCLTIPVAFGVYVNYRW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAIVAQYGIMPLSAFLLGKVFHLTSIEALAILICGCSPGGNLSNLFTLAMKGDMNLSIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPFNES---LPPGEG-HRATDTALSVILVVMLLLIMLSLGCTMEFSKIKAHFWKPKGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
  HGNLELVFTVVSTVMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAAYOTYKRRLKNKHGK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALFTHQSWQRCRTISLETGAQNIQMCITMLQLSFTAEHLVQMLSFPLAYGLFQLIDGFLI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCSSFTALGMMPLLLYIYSKGIYDGDLKDK--VPYKGIMLSLVMVLIPCAIGIFLKSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYVPYVLKAGMIITFSLSVAVTVLSVINVGNSIMFVMTPHLLATSSLMPFTGFLMGYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKQSKIILKIGAVVGGVLLLVVAVAGVVLAKGSWNSDIT--LLTISFIFPLIGHVTGFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 21,
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 546; DB 11;
larity 37.2%; Pred. No. 4.5e-37;
Conservative 70; Mismatches 117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                           46503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; bass; 1.
34886 MW;
                                                                      27.0%;
35.7%;
                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                      Score 535;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                           055E989629CC13D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA32C829C8A8E6D0
                                                Mismatches
                                                                      5e-36;
                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                              101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                              databases
                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                          Length 437,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 317;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                40;
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                                              Gaps
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Query Match
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
9nknown (Protein for IMAGE:3502817) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96EP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96EP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01758; SBF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC012048; AAH12048.1; -.
Pro; IPR002657; BileAc/Na_smprtr
4
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                                                                                                                                                                                                                                                                                                                                                                                   LYTWSW---SLOQULTIPYQNIGITLVCLTIPVAFGVYVNYRWPKQSKIILKI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHLPPNCKRTVCLETGSQNVQLCTAILKLAFPPQFIGSMYMFPLLYALFQSAEAGIFVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQTYKRRLKNK 318
                                                                                                                                           THQSWQRCRTISLETGAQNIQMCITMLQLSFTAEHLVQMLSFFLAYGLFQLIDGFLIVAA
                                                                                                                                                                                                                            TLVVLFIMTGTMLGPELLASIPAAVYVIA--
                                                                                                                                                                                                                                                                                                                                   IYSWAWINTPIVQ--LLPLGTVTLTLCSTLIPIGLGVFIRYKYSRVADYIVKVSLWSLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGLNVFVGAALCITMLG-----LGCTVDVNHFGAHVRRPVGALLAALCQFGLLPLLAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNLELVFTVVSTVMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THOSWORCRTISLETGAONIOMCITMLOLSFTAEHLVOMLSFPLAYGLFOLIDGFLIVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYTWSW----SLQQNLTIPYQNIGITLVCLTIPVAFGVYVNYRWPKQSKIILKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGLNVFVGAALCITMLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALAFKLDEVAAVAVLLCGCCPGGNLSNLMSLLVDGDMNLSIIMTISSTLLALVLMPLCLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AISFSLKPVQAIAVLIMGCCPGGTISNIFTFWVDGDMDLSISMTTCSTVAALGMMPLCIY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQTYKRRLKNK 318
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                                    <del>..</del>
                                                                                                                     FHLPPNCKRTVCLETGSQNVQLCTAILKLAFPPQFIGSMYMFPLLYALFQSAEAGIFVLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                              GAVVGGVLLLVVAVAGVVLAKGSWNSDITLLTISFIFPLIGHVTGFLLALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%;
35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 535; DB 4;
Pred. No. 5.3e-36;
9; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
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ON THE PROPERTY OF THE 
                                                                                                                                           RESULT 9
08022
ID 08020
AC 08020
DT 01-J-DT 01
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Best Local S
Matches 64
                                       Matches
                                                                Query Match
Best Local Similarity
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Q8VI83;
Q8VI83;
01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-JUN-2002 (TrEMBLrel. 21, L
Ileal sodium-dependent bile a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8QZR2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Similar to protein P3 (Hypothetical 50.3 kDa prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Saeki T., Kirifuji K., Kanamoto R., Iwami K.;
"Identification of transcription start sites i
dependent bile acid transporter gene.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AB078635; BAB84081.1; ...
                                                                                                                                                                                             Submitted (APR-2002) to the EMBL; BC023050; AAH23050.1; EMBL; BC027440; AAH27440.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8QZR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                              Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                              Strausberg
                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                        Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Pfam; PF01758; SBF; 1.
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473 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                              50254 MW;
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                                                                Score 351.5; DB 1
Pred. No. 6.4e-21;
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Pred. No. 1
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Matches 80
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Q9QZJ2;
01-MAY-2000
       Q9BSL2;
Q9BSL2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Balasubramanian N., Arrese M., Suchy F.J., Ananthan "Na-Taurocholate cotransporting polypeptide (Ntcp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Na-taurocholate cotransporting polypeptide (Fragment).
Mesocricetus auratus (Golden hamster).
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187 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 351;
Pred. No. 2.
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                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2855C5F44AB482C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                          448
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
2.8e-21;
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Best Local S
Matches 87
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
Bacillaceae; Bacillus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2001) to the
                                                                                                                                                                                                     SEQUENCE FROM N.A.
Lapidus A., Galleron
Submitted (NOV-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 034524
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TIGRFAMs; TIGR00841; bass; 1.
SEQUENCE 448 AA; 47548 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to protein P
Homo sapiens (Human)
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                     STRAIN=168
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                        Putative transporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004710; Bass.
InterPro; IPR002657; BileAc/Na_smprtr.
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Pred. No. 1.8e-19;
3; Mismatches 115;
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320

241

371

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260

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RESULT
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AC Q9
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Best Local S
Matches 84
                              099RV2;
099RV2;
01-JUN-2001
01-JUN-2001
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AF027868, AAB84443.1; -
EMBL; Z99114; CAB13827.1; -
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SEQUENCE 321 AA;
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InterPro; IPR002657; BileAc/Na_smprtr.
Pfam; PF01758; SBF; 1.
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                                                                                                                                      PRELIMINARY;
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                                    17,
17,
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; Pred. No. 6.5e-19;
76; Mismatches 114;
                                    Last sequence update)
                                                                      Created)
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RESULT 14
Q8YIU6
ID Q8YIU
AC Q8YIU
DT 01-M2
DT 01-J1
DE Sodi:
GN BMEI
OS Bruc
OC Bact
OC Bact
OC Bruc
OC NCB;
RN [1]
RN [1]
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Best Local S
Matches 68
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01-MAR-2002
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                       Q8YIU6;
                           SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / BIOTYPE
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP003365; BAB58483.1; -.
EMBL; AP003136; BAB43413.1; -.
InterPro; IPR002657; BileAc/Na_smprtr.
Pfam; PF01758; SBF; 1.
Hypothetical protein; Complete proteom
SEQUENCE 305 AA; 32865 MW; 1E42301:
                                                                                                                                             Brucellaceae; Bru
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                         Sodium/bile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SAV2321. SAV2321 OR SA2112.
                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                            Brucella melitensis.
                                                                                                                                                                                                                                                     BMEI 0346.
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          Anderson
                                                                                                                                                                                                                                                                            acid cotransporter homolog, SBF
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                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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05 AA; 32865 MW; 1E423015196B6657
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                                                                                                                                                                              Brucella
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27.9%;
     l V., Redkar R.
Bhattacharyya
                                                                                                                                                                                                  alpha subdivision; Rhizobiaceae
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Pred. No. 5.3e-17;
0; Mismatches 101;
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       Patra G., M
Lykidis A.,
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family.
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I., Kaito C.,
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Best Local S
Matches 79
                                                           Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                                                                           Complete proteome. SEQUENCE 323 AA;
                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilia Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001510; BAB04577.1; -.
EMBL; PR002657; BileAc/Na_smprtr.
                                                                                                                                                                                                                                                                                                 STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
Bacillaceae; Bacillus.
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01-MAR-2002
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01-OCT-2000
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                                                                                                                                                           Pfam; PF01758; SBF;
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Fuji F., Hirama C., Nakamura Y., Ogasawara N
                                                                                                                                                                                                                                                         forikoshi
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| FAPWIVVLLGIIMEGMGLTISGKDFAEVAKRPFDVAIGVLAQFIIMPLLAVLLTRIIPM
FTWITPHITILLGVIMFGMGLTLKLSDFRIVLQKPIPVLVGVLAQFVIMPLVAFALAYAF
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                            FTVVS----TVMMGLLMFSLGCSVBIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLLAISF
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                                                         15.1%; Score 299.5; DB 16; llarity 24.8%; Pred. No. 8.2e-17; Conservative 80; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                           AA;
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                                                                                                                           34259 MW;
                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15, Created)15, Last sequence update)20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SGLLIFAVVVLHNCCGLLLGYFAARFAGLSLAKRKAISIEVGMON
                                                                                                                           4434161552137F97 CRC64;
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                                                                                                                                                                                                                                                                     Ogasawara N.,
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                                                                                          DB 16;
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                                                                                                                                                                                                                                                                     Sasaki R., Masui N., ., Kuhara S.,
                                                             Indels
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